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February 16, 2003, 15:50:54; Search time 2492.14 Seconds (without alignments) 16465.781 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                           2054640 seqs, 14551402878 residues
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Maximum Match 100%
Listing first 45 summaries
                                               OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Variation in primary sequence and tandem repeat copy number among 1-antigens of Ichthyophthirius multifilis
Mol. Biochem. Parasitol. 120 (1), 93-106 (2002)
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llarity 72.3%; Pred. No. 3.8e-220;
Conservative 0; Mismatches 391;
                                                         1 (bases 1 to 3026)
Lin,Y., Lin,T.-L. and Clark,T.G.
Direct Submission
Submitted (27-NOV-2000) Microbiology and University, Ithaca, NY 14853, USA
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3 (bases 1 to 2486)
3 (bases 1 to 2486)
Dirkf. G., Lin, T.-L., Jackwood, D.A. and Dickerson, H.W.
Direct Submission
Submitted (29-MAR-1999) Microbiology & Immunology, Cornell
University, College of Veterinary Medicine, Ithaca, NY 14853, USA
Location/Qualifiers
                                                                                                                                                                                                      The gene for an abundant parasite coat protein predicts tandemly repetitive metal binding domains Gene 229 (1-2), 91-100 (1999) 99196987
                                                                                                                                                                                                                                                                                       (bases 1 to 2486)
Gaertig, J., Gao, Y., Tishgarten, T., Clark, T.G. and Dickerson, H.W.
Surface display of a parasite antigen in the ciliate Tetrahymena
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                                                                                Ichthyophthirius multifiliis.
Ichthyophthirus multifiliis
Ichthyophthirus multifiliis
Eukaryota, Alveolata; Cillophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
1 (bases I to 2486)
Clark, T.G., Lin, T.L., Jackwood, D.A., Sherrill, J., Lin, Y. and Dickerson, H.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="IAG48"
/product="immobilization antigen precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="surface protein; 48 kDa i-antigen"

    2486
    /organism="Ichthyophthirius multifillis"
/serotype="A"

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399. .1845
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399. .1845
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/gene="IAG48"
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/gene="IAG48"
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Best Local 9
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AF405431 1520 bp mRNA linear INV 27-FEB-2002 Inthyophthirius multifillis 52kDa immobilization antigen variant B
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Direct Submission
Submitted (0.1-Aug.-2001) Microbiology and Immunology, NYSCVM Cornell University, Ithaca, NY 14853, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPEVPNYSSPNGCVACOVNKSDSQLRPGAQANLATQCNNECPFGTA LODGAFFITYO
SISOCTFCKVDFYFNGNPSAQNPGNGOFFPGQLIANPDAATAAQIPMVPGPNSKCVA
CESKKTNSQSRSGLEANLAAQCGFPGFGTLVTGVTVTVSLSQCVNCKAGFPYONS
NFEAGKSQCNKCAVSKTGSASPPGNATSATQCOUNCPAGTVVDDGTSTNFVALASE
TKCQANFYASKTSGFAAGTDTCTECSKKLTSGATAKVYAEATQKAQCASSTFAKFLSM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Variation in primary sequence and tandem repeat copy number among tantigens of Ichthyophthirius multifillis Mol. Blochem. Parasitol. 120 (1), 93-106 (2002) 21839613
                                                                                                                                                                                                                                                                                                                                                                          Ichthyophthirius multifiliis.
Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
1 (bases 1 to 1520)
Lin, Y., Lin, T.L., Wang, C.C., Wang, X., Stieger, K., Klopfleisch, R. and Clark, T.G.
1114 GCTACCCTGATCGCTCAGTGTGCTCTGGAGTGTCCTGCTGGAACCGTGCTGACCGACGGA 1173
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                                                                   4.1%; Score 57.2; DB 3; Length 1520; 52.0%; Pred. No. 2.5e-05; Live 0; Mismatches 138; Indels 9

    1520 / Organism="Ichthyophthirius multifiliis"

                                                                                                                                                                 1683 AAAAGTATAATGCGCCTCCACTACTTTC 1710
                                                                                                                                           GAACATCCAGTGTGACTTCGCTAACTTC 1365
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/note="IAG52B[G5]"
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AF405431
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/isolate="G5"
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1155 AACCGTGCTGACCGACGGAACCACCTC 1181
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/product="junctophilin 3"
/protein_id="AAL40941.1"
/bc.kref="61:17646245"
/translation="MSSGGRENFDDGGSYCGGWEDGKAHGHGVCTGFKGQGEYTGSWS
/translation="MSSGGRENFDDGGSYCGGWEDGKAHGHGVCTGFKGQGEYTGSWS
HGFFVLGVYTWPSGNTYQGTWAQGKRHGIGLESKGKWVYKGEWTHGFKGRYGVRECAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 125020)
Holmes,S.E., Ingersoll-Ashworth,R.G., Ross,C.A. and Margolis,R.L.
Direct Submission
Submitted (05-0CT-2001) Psychiatry, Johns Hopkins Medical
Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 125020)

Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hwang, H.S., Ingersoll. Ashworth, R.G., Fleisher, A., Stevanin, G., Brice, A., Potter, N.T., Ross, C.A. and Margolls, R.L.

A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2

Nat. Genet. 29 (4), 377-378 (2001)
                                                                                 CTGACCTCTGGAGCTGAGGCTAACCTGCCTGAGTCTGCTAAGAAGAACATCCAGTGTGAC 1353
                                                                                                                                                 ACCACCTCTACCTACAAGCAGGCTGCTTCTGAGTGTGAAGTGTGCTGCTAACTTCTAC 1233
                  ACCACCAAGCAGACCGACTGGTGGCTGGAATCGACACCTGTACCTTGTAACAAGAAG 1293
                                                                                                                                                                                             -----TTCGCTAACTTCCTGTCTATCTCTGCTGCTGATCTCTTACTACCTGCTG 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /map="16q34.3; between D168520 and WI-12410"
/note="isolated from a patient with Huntington's
Disease-Like 2 (HDL2)"
complement(35581. .35746)
/rpt_type=tandem
/rpt_unit=ctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens junctophilin 3 (JPH3) gene, partial cds.
AF429315
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/gene="JPH3"
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/gene="JPH3"
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/db_xref="taxon:9606"
/chromosome="16"
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GMRMMGSASSRRCKSASRSSWCSRRMKGMRGSCWSSKMWGGSRSRSASSKCKGSRGMRRR 17705
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                                                                                                                                                                                                                                                                                                                                                        16988 YASWCCMCCWCCMRSCCCMRSYCCCMRSYCCMRSSYWTMSASYMSRRSYWKRSM 17047
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                                                                                                                                                                                                                                                                                                                     259 CTGGTGACCCAGTGTAACGTGAAGTGTCCTGCTGGAACCGCTATCGCTGGAGGAGGTACC 318
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                                                                                                                                                                                                              ACCCCTTGTCCTCAGAAGAAGGACGCTGGAGCTCAGCCTAACCCTCCTGCTACCGCTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17106 RKMKMYSSKGMYCWYCWCWGRRGCYCSCWTSRSAMCCSYCYAKCKSMCYSCYYGMSMKGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17286 SMASRGMSWSSYMKMMKSSWRMSCYMKCCWCMKMCYCMMRSMRSRGMSYYMYASWKSSSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                736 ATCTCTGCTGCTGGAGTGAACAACTGGGTGGCTCAGAACACCGAGTGTACCAACTGTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGTCCTGCTAACAAGGACTACGGAGCTGAGGCTACCGCTGGAGGAGCTGCTACCCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                               319 GACTACGCTGCTATCATCACCGAGTGTGTGAACTGTCGCATCAACTTCTACAACGAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAGCTCTGACCGCT - - - GGAAACGCTGCTACCATCGTGGCTCAGTGTAACGTGGCTTGT
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                                                                                                                                                          9
                                                                                                    Length 125020,
                         4254 others
                                                                                                                                                             Conservative 421; Mismatches 452;
                                                                                                          DB 9;
                                                                                                    Score 55.2; DB 9 Pred. No. 0.00014
NGAKYEGTWSNGLQDGYGTETYSDG"
1 32731 c 30696 g 28283 t
                                                                                                          3.9%;
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D 1109480/0
E 2 (bases 1 to 125020)
S Holmes, S.E., Ingersoll-Ashworth, R.G., Ross, C.A. and Margolis, R.L.
Direct Submission
L Submitted (OS-OCT-2001) Psychiatry, Johns Hopkins Medical
Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
I Location/Qualifiers
Ince //organisme"Homo sapiens"
/db_xref="taxon:9606"
/chomosome="16"
/map="lisolated from a patient with Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRI 18-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 12502)

Holmes,S.E., O'Hearn,E., Rosenblatt,A., Callahan,C., Hwang,H.S.,

Ingersoll-Ashworth,R.G., Fleisher,A., Stevanin,G., Brice,A.,

A repeat expansion in the gene encoding junctophilin-3 is

sascidated with Huntington disease-like 2

21583737
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                                                                                                                                            1098 TACCGCTGGAGGAACCGCTACCCTGATCGCTCAGTGTGTCTCGAGTGTCCTGCAGAAC 1157
                                                                                                                                                                          956 TGCTCCAGGTAATACTGCTACTTAAGCCACATAATGTTTGACCACATGTCCTGCTGGTAC 1015
                                                                                                                                                                                                              1158 CGTGCTGACCGACGGAACCACCTCTACCTACAAGCAGGCTGCTTCTGAGTGTGTGAAGTG 1217
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                                                                                                                   Gaps
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AP429315
AF429315 GI:17646244
                                                                                                                 Indels
                                                                              Score 52.2; DB 3;
Pred. No. 0.00075;
); Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                1278 CTCTTGTAACAAGAAGCTGACCTCTGGAGCTGAGGCT 1314
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                                401
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complement(<36507. .36887)
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complement(35581. .35746)
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/product="junctophilin 3"
              /rpt_unit=414..680
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                                                                                                              Conservative
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Clark, T.G., McGraw, R.A. and Dickerson, H.W.
Developmental expression of surface antigen genes in the parasitic
ciliate Ichthyophthirius multifillis
Proc. Natl. Acad. Sci. U.S.A. 89 (14), 6363-6367 (1992)
                                                                                                                                                                                              ichthyophthirius multifillis.
Ichthyophthirius multifillis
Ichthyophthirius multifillis
Bukaryota; Alveolatu; Cillophora; Oligohymenophorea;
Bukaryota; Ophryoglenina; Ichthyophthirius.
I (bases 1 to 1249)
Lin, T.L. and Dickerson, H.W.
Purification and partial characterization of immobilization antigens from Ichthyophthirius multifillis
J. Processol. 39 (4), 457-463 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (18-SEP-1998) Microbiology and Immunology, Cornell University, Ithaca, NY 14853, USA Sequence update by submitter on Sep 18, 1998 this sequence version replaced gi:159289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (06-JUN-1992) Microbiology and Immunology, Cornell
University, Ithaca, NY 14853, USA
(bases 1 to 1249)
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6. .1187
/product="immobilization antigen"
DD 17826 KMYMWRAACMMYCYMSTRRMMCMMSMC 17852
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/transl_table=6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="Georgia"
/db_xref="taxon:5932"
/dev_stage="trophont"
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/rpt_type=tandem
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/citation=[1]
                                                                                                                                                                 M92907.1 GI:3628568
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                                                                                                                                 mRNA, partial cds. M92907
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/protein_id="AAL40941.1"
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//tb_xref="G1:17646245"
//tb_xref="G1:17646245"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCMCKSCCGCYSMGMSSYSYSGKYSWGMKSYMWRSYYSKRSTSKAWRSSKRCMGTGGRYK 17016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17424 RCCMKKGCTGYRGMSSKKSGYKSMRGMRGSSYSTSCWKSCWGYSWMKCMKYMSYKKKRR 17365
                                                                                                                                                                                                                                                          17784 AGSKSSRGGTGYYMKKKGGGKGSMSSKKWKGSSTSRRGSSAKSCSYMWGMSMCMSCMSM 17725
                                                                                                                                                                                                                                                                                                                         17724 AKSYMMCYCYMYRMSSYMSYYKCYSCMGMSSTSYSCCWKMSSWGSCYKCMKYYSGWS 17665
                                                                                                                                                                                                                                                                                                                                                                                                  SYSTSMGYYSSTSCKKYKCSWSSMYKCKTSKSYRRRRSYYWGGGKRAKKKYYCAGRRRR 17605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17544 YCMMRSSKSSSWSMSMSMCMGWGGGGYRRSKRSAGWCAGWRSSKGKRSTGMKRACSKK 17485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTTCTCGCTGTAAGGCTTGTCCTGCTAACAAGGTGCAGGGAGGTGTGGCTACCGCTGGA 1107
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                                                                                                                                                                                     Gaps
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                                                                                                                                           Length 125020,
                                                                                            4254 others
                                                                                                                                               ch 3.5%; Score 50; DB 9; Length 125
1 Similarity 10.1%; Pred. No. 0.0049;
93; Conservative 409; Mismatches 406; Indels
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Matches 93; Conserv
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Consensus quality: 217356 bases at least Q40
Consensus quality: 22317 bases at least Q30
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Consensus quality: 224119 bases at least Q30
Consensus quality: 224119 bases at least Q30
Estimated insert size: 258000; agarose-fp estimation
Estimated insert size: 25872; sum-of-contigs estimation
Quality coverage: 7.65 in Q20 bases; agarose-fp estimation

* NOTE: This is a 'working diaft' sequence. It currently

* consists of 19 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are uknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                   AC073693 230372 bp DNA linear HTG 29-JUN-2000
Mus musculus clone RP23-152L22, WORKING DRAFT SEQUENCE, 19
                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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Center: Joint Genome Institute
Center Code: JGI
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Mammalia, Eutheria, Rodentia,
I (bases 1 to 230372)
DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                       166 GCTGCTGCTTTCGTGCCTGGGGCTTCTACCTGTACCCCTTGTCCTCAGAAGAAGGACGCT 225
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                                                                                                                                                                                                                                                                                                                                                                         3.1%; Score 43.4; DB 2; Length 230372; 53.9%; Pred. No. 0.46; Live 0; Mismatches 76; Indels 0;
      80284: contig of 14664 bp in length 80384: gap of unknown length 89849: gap of unknown length 16562: contig of 17713 bp in length 16562: contig of 17713 bp in length 140706: contig of 24344 bp in length 140806: gap of unknown length 16769: contig of 24344 bp in length 16769: contig of 26803 bp in length 167799: gap of unknown length 16799: gap of unknown length 199398: contig of 31689 bp in length 19498: gap of unknown length 230372: contig of 30874 bp in length
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53740 c 52522 g 61042 t 1802 others
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Pearman,C., Meyer,R. and Doebber,A.
The sequence Hamo sapiens BAC clone RP11-582C12
Unpublished (2001)
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                                                                                                                                                                                                                                                          /organism="Mus musculus"
                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                             /clone="RP23-152L22"
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Sulston, J.E. and Waterston, R.
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gap of
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Waterston, R.H.
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Waterston, R.H.
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Matches 89; Conservative
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Direct Submission
Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 159764)
                                                                                                                                                                                                                                                                                        Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA ON Nov 17, 2001 Lis sequence version replaced 91:15887350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.Y., (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Louis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. 1 MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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137. .299
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302. .653
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2 (bases 1 to 643)

2 (bases 1 to 643)

2 (bases 1 to 643)

Direct Submission

Submitted (27-APR-2001) Oceanography, University of Washington, Box

357940, Seattle, WA 98195-7940, USA

357940, Docattle, WA 98195-7940, USA

1. 643

1. 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thalassiosira weissflogii isolate CCMP 1336 clone 10 sexually induced protein SIG 1 gene, partial cds.
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Rapid evolution of a sexual reproduction gene in centric diatoms of the genus Thalassiosira
Appl. Environ. Microbiol. 67 (8), 3501-3513 (2001)
21365169
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Thalassiosirophycidae; Thalassiosirales; Thalassiosiraceae;
Thalassiosira.
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24843. 25094
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Thalassiosira weissflogii
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24291. .24321
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Best Local Similarity 52.6
Matches 90; Conservative
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1 (bases 1 to 179217)

8 Akhter. N. Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Idol. J.R., Karlins, E., Laric, P., Margulies, E. H., Masleilo, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Netherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
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TCMTIEQGLAFLDHYDLMSDFDRDYME"
163 c 144 g 170 t
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Bos taurus clone RP42-504H16, WORKING DRAFT SEQUENCE, 5 ordered
                                                                                                                                                                                                                                                                                                                                                                                 278 TGAAGTGTCCTGCTGGAACCGCTATCGCTGGAGGAGCTACCGACTACGCTGCTATCATCA
                                                                                                                                                                                                                                                                                                                                                                                                         338 CCGAGTGTGTGAACTGTCGCATCAACTTCTACAACGAGAACGCTCCTAACTTCAACGCTG 397
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join(<1. .56,141. .>643)
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join(<1. .56,141. .>643)
/codon_start=2
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                                                                                                                                                                                                                                                                                                     2.9%; Score 41; DB 8; Length 643; 55.2%; Pred. No. 1.4;
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AC099748.2 GI:21427692
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Web site: http://www.nisc.nih.gov

Contact: nisc_zoo@nhgri.nih.gov

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The sequence data in this record represents an 'enhanced' version of a phase 2 submission. Specifically, the indicated order and orientation of each sequence contrig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least BX average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990119
Consensus quality: 177994 bases at least Q40
Consensus quality: 177874 bases at least Q20
Insert size: 136000; agarose-fp
Insert size: 178817; sum-of-contigs
Quality coverage: 12.94x in Q20 bases; sum-of-contigs
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/note="clone overlaps with GenBank Accession Number AC113228 clone RP42-67B23 (center project name crl)" 38501 c 36655 g 49899 t 400 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by the finished sequence as soon as it is available and the accession number will be preserved.

32314: contig of 33314 bp in length
32415 32414: apa of unknown length 66137 66236: gap of unknown length 66337 80633: contig of 14397 bp in length 66237 80633: contig of 14397 bp in length 80634 80733: gap of unknown length 80734 92700: contig of 11967 bp in length 92701 92800: gap of unknown length 92701 92800: gap of unknown length
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/note="assembly_fragment"
66237 .80633
/note="assembly_fragment"
80734 .92700
/note="assembly_fragment"
Project Information
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/note="assembly_fragment
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/note="assembly_fragment
                             Center project name: crq
Center clone name: 504H16
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/db_xref="taxon:9913"
/clone="RP42-504H16"
/clone_lib="RP42"
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                       Center project name:
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Thalassiosira
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NDIILAGSTLYPYGTTEGFPLMSGTAGTVIANTAHDYMECSNKGLCDRINGLCECLPG
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TCMTIEQLALDLAFLDHYYDLMDKDYTMGCKCDPGYTGP"
146 c 144 9 149 t
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Direct Submission
Submitted (27-APR-2001) Oceanography, University of Washington, Box 357940, Seattle, WA 98195-7940, USA
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The (bases 1 to 591)

Armbrust.B.V. and Galindo, H.M.

Rapid evolution of a sexual reproduction gene in centric diatoms of the genus Thalassiosira

Appl. Environ. Microbiol. 67 (8), 3501-3513 (2001)
21365169
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                                                              Db 106730 recraagreerreagreergreegacrergrergacreearagaaggeageeceecagg 106789
                                                                                                                                                                                                      Db 106790 CICCCCCAICCCIGGGAITCICCAGGCAAGAACACIGGAGIGGGITGCCAITICCITCIC 106849
                                                                                                                                                                         963 AGCIACCAACTACGIGAICCIGCAGACCGAGIGICTGAACIGIGCTGCIAACIICIACII 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thalassiosira weissflogii.
Thalassiosira weissflogii
Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
Thalassiosirophycidae; Thalassiosirales; Thalassiosiraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                338 CCGAGTGTGTGAACTGTCGCATCAACTTCTACAACGAGAACGCTCCTAACTTCAACGCTG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  278 TGAAGTGTCCTGCTGGAACCGCTATCGCTGGAGGAGCTACCGACTACGCTGCTATCATCA 337
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                                                                                                           TGCTACCCTGGCTAAGCAGGTGAACATCGCTTGTCCTGACGGAACCGCTATCGCTTCTGG 962
                                            TACCTGTCTGCCTTGTCCTGCTAACAAGGACTACGGAGCTGAGGCTACCGCTGGAGGAGC 902
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/protein_id="AAK70420.1"
/db_xref="GI:14586995"
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               Indels
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/isolate="CCMP 1336"
/db.xxef="taxon:67004"
/clone="13"
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Pred. No. 4.3;
               100;
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2.3;
 Pred. No. 2.3;
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                                                                                                                                                                                                                                             1023 CGACGGAAACAACTTCCAGGC 1043
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 50.2%;
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nes 79; Conservative
                    Conservative
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   Local Similarity
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/translation="SHDMCTCDRNFOGADCSLRTCPFGKAHVDTPRGDLDASLTIGDH
NDIIIAGPTLYPYGTTEGLPLMSDTAGTVIANTAHDYMECSNKGLCDRINGLCECLPG
YDGAACQRASCPSKANYSTPGSGQGERSNTNFKVFNANSAFHGRAADVVQRDQCSGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Armbrust, E.V. and Galindo, H.G.
Direct Submission
Submitted (27-APR-2001) Oceanography, University of Washington, Box 357940, Saattle, WA 98195-7940, USA
Location/Qualifiers
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Rapid evolution of a sexual reproduction gene in centric diatoms the genus Thalassiosira
Appl. Environ. Microbiol. 67 (8), 3501-3513 (2001)
21365169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257
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                                                                                                                                                                                                                                                                                                                                                                                                                          Coscinodiscophyceae;
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258 ATAAGGGATTATGCGATCGCTTCAGCCTTTGCGAATGTCTTCCTGGCTATGACGGTG 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 CCTGTACCCCTTGTCCTCAGAAGAAGGACGCTGGAGCTCAGCCTAACCCTCCTGCTACCG
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Thalassiosirophycidae, Thalassiosirales, Thalassiosiraceae,
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/product="sexually induced protein SIG
join(<1. 56,141. >643)
/codon(<1. 56,141. >643)
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/isolate="CCMP 1336"
/db_xref="taxon:67004"
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48.0%; Pred. No. 7.4;
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162 c 147 g 168 t
                                                                            422
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Thalassiosira weissflogii
                                                                                                                        318 CAGCTTGCCAGCGTGCATCATGTCC
                                                                                                                                                                                                                                                                                                                                         AF374492.1 GI:14336347
                                                                            GAGCTICTACCTGIACCGCTIGICC
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6858. 6911,7028. 7081,7421. 7474,7563. 7607,7724. 7777,7892. 7936,8115. 8168,8426. 6824,8612. 8656,8760. 8858,8990. 9043,9261. 9368,9444. 9517,9643. 9741,9907. 9960,10049. 10147,11045. 11098,11242. 11295,11399. 11452. 11564. 11617,12068. 1212,12206. 11295,11399. 11452. 11569. 11679. 11479. 11479. 11479. 11479. 14712,1459. 11479. 14717,13466. 13549,13712. 113765,13983. 14090,14179. 11588.15296. 15349,15454. >15561)
//codon start=1 //product="collagen type I alpha 1" //protef="collagen type I alpha 
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4168. .4362

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/number=2

4501. .4535

/gene="COLIAI"

/number=3

4501. .4535

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/gene="COLIAI"

/number=3

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/number=3

4601. .4637

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/number=6
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/gene="COL1A1"
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/gene="COL1A1"
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2484. 15561
2486. 2460
2484. 15561
2484. 2705,4168. 4362,4501. 4535,4638. 4673,
90in(2484. 2705,4168. 4362,4501. 4535,4638. 4673,
90in(2484. 2705,4168. 5931,6090. 6143,6306. 6359,6358. 6911,7028. 7081,7421. 7474,7563. 7607,7724. 7777,
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8990. 9043,9261. 9368,9464. 9517,9643. 9741,9907. 9960,
11049. 11045. 111098,11242. 11295,11399. 11452,
11564. 11617,12068. 12112,12206. 12304,12602. 12709,
13168. 13375,13496. 13549,13712. 13765,13983. 140990,
14179. 115188,15296. 15349,15454. >15561)
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1 (bases 1 to 16814)
Simon,M.P., Pedeutour,F., Sirvent,N., Grosgeorge,J., Minoletti,F., Coindre,J.M., Territar-Lacombe,M.J., Mandahl,N., Craver,R.D., Fransson,I., Guilbaud,C. and Dumanski,J.P., Redra,D., Persepliation of the platelet-derived growth factor B-chain gene via and glant-cell fibroblastoma COLIA1 in dermatofibrosarcoma protuberans Nat. Genet. 15 (1), 95-98 (1997)
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4764. .4865,5588. .5659,5887. .5931,6090. .6143,6306. .6359,
                                                                                                                                                             HSCOLPDGF 16814 bp DNA linear PRI 12-MAR-1997
H.sapiens DNA sequence of COLIA1 gene fused with intron 1 of PDGFB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (21-JUN-1996) K.P. O'Brien, Dept. of Molecular Medicine,
Clinical Genetics Unit, Karolinska Hospital, Building L-6, S-171 79
Stockholm, SWEDEN
                                                                                                                                                                                                                                                                                           X98705
X98705.1 GI:1888408
COLIA1 gene; collagen alpha 1 type I; PDGFB gene; platelet-derived
growth factor beta; translocation breakpoint.
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/db_xref="taxon:9606"
/clone_llb="cosmid D4"
/note="chimaeric cosmid clone spanning a translocation proceam between COLIA1 gene fused with intron 1 of PDGFB gene"
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Location/Qualifiers
Location-"Homo sapiens"
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15831, 16814
Organism="hono sapiens"
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/gene="COL1A1"
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O'Brien, K.P.
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Homo sapiens
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gene
                                                       RESULT 13
HSCOLPDGF/C
LOCUS
DEFINITION F
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MEDLINE
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AUTHORS
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KEYWORDS
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YHLKTGCOWNMLPGDPPPSSTVYSYYRKWORKGVWEKLNHTLRGOVRAKLGKSTQPSA
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                                                                                                                                                                                                                   BCT 28-NOV-2001
                                                    Kaneko,T., Nakamura,Y., Wolk,C.P., Kuritz,T., Sasamoto,S., Watanabe,A., Iriguchi,M., Ishikawa,A., Kawashima,K., Kimura,T., Kishida,Y., Kohara,M., Matsumoto,M., Matsuno,A., Muraki,A., Nakazaki,N., Shimpo,S., Sugimoto,M., Takazawa,M., Yamada,M., Yasuda,M. and Tabata,S.
8448 GCCCCTTGGGGACCAGCTTCACCCTGAATCAGAAGAAAGGACATATCAGAAGCCACCCTG 8389
                               620 GAAAGTUTCAGTGTACCCCTTGTCCTGCTATCAAGCCTGCTAACGTGGCTCAGGCTACCC 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (02-MAY-2001) Takakazu Kaneko, Kazusa DNA Research
Institute, The First Laboratory for Plant Gene Research; Yana
1532-3, Kisarazu, Chiba 292-0812, Japan
(E-mail:kaneko@kazusa.or.jp,
URL:http://www.kazusa.or.jp,
Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3934)
Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3934)
                                                                                                                                                                                                                 AP003600 341950 bp DNA linear BCT 28-NON
Nostoc sp. PCC 7120 plasmid pCC7120alpha DNA, complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120
DNA Res. 8 (5), 205-213 (2001)
21595285
                                                                                                                                                                                                                                                                                                                 Nostoc sp. PCC 7120 plasmid:pCC7120alpha DNA.
Nostoc sp. PCC 7120
Bacteria; Cyanobacteria; Nostocales; Nostocaeee; Nostoc.
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complement(165..548)
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AP003600.1 GI:17135339
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46.7%; Pred. No. 9.7;
Live 0; Mismatches 139; Indels 0;
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6912. 7027

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7937. 8114
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8426. 8524
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Best Local Similarity 46.7
Matches 122; Conservative
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LIEKMORKVTVTFNGEEDHYHLLFQYHPDVELSKLVNNLKSVSSRKLRQEFABHLESFY
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complement(5798..7252)
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similar to hemolysin export system membrane fusion protein
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TVKIQAYFHQSNSHHQIEYGDITLNTEQVQAVWMRRLWQPHLSPELAPQYRDACTKES
TAVWDGFWDSIRHAHWYDDLQKINAAENKLYQLAVAAEVGLVIPPTLYTNNNFEAREF
FEQNNGKWNTKLLKFLSYSMEGSSFFWYTSTVKEEDLLDAFTLRYCPWYGAQIPKQO
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ELRAVYNMITKLLKFLSYSMEGSSFFWYTSTVKEEDLLDAFTLRYCPWYGAQIPKQO
GLTFGAFDFIYTPLEEYVFLEINPTGEWGMLERDLNYPISEAIADSLIQN"
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                                                                                                                                                                                                                                                                                                                               /protein_id="BAB78093.1"
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complement(9429, .9731)
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hypothetical protein"
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                                                                        5254. .5673
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5254. .5673
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Matches 152; Conservative
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MLRYHQRRCTGRKVAPSSLVIRGSVKLACAIATKLHSFTASDLAQVDIHTWLELRSQL
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NEDLVALLEVANTLAVPIDGVVSDGQOSIRRAVGLAFRIAHGLCHYHYLKEAIKPI
YEADRNAKKELKKKS"
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3776. .4126
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DRIAAPKFLKKAAERKLKLAORKYSRRKKGSNRRKKAIQQLGKQHKKVADTRKDFHYKT
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EPAKGSRKNASLRVSSSHRPLTPSRVTALVLRRPELI"
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Complement(2527. .3228)
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Length 224271;

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Direct Submission

L Submitted (24-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Direct Submission

L Submitted (01-JUL-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

E 4 (bases 1 to 224271)

E 6 (Dases 1 to 224271)

E 7 (Dases 1 to 224271)

E 8 (Dases 1 to 24271)

E 9 (Dases 1 to 24271)

E 9 (Dases 1 to 24271)

Direct Submission

L Submitted (16-JUL-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Jul 16, 2002 this sequence version replaced gi:21637469.

Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-spic.stanford.edu
duality: Phrap Quality >=40 99.3% of Sequence;
Estimated Total Number of Errors is 0.9.
NOTE: This insert is not the entire sequence of the clone (entire sequence is 23xbb). It is clipped at the overlap with AC009002. The number of bases overlapped is 5260.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                           Db 326556 TGTGAAGGTGAGAGGGTTTTATCGGTGGTAATTTGACTACCTGTGTTCAGGGTGACGGT 326497
                                                                                                                                                                                                                                                                                                                                                                                                                            DD 326496 AACATCAGGGTTGGGTTGGGTTCTCAGAACTAGGGTGTAACTGTCAGTGTTACCACCTTC 326437
DD 326736 CCCGCGAATTTCGGCATCGTTATCAGTGATGCTGACACAATATCGGGGAGAGATAACATT 326677
                                                                                                                                                                                                                      DD 326616 GGTTATGGTGGTTAACTGCGTTAACGGTTATTGGTGGAGTATCCAGTTAGCGGA 326557
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                                                                                                                                                                                  241 CCTCCTGCTACCGCTAACCTGGTGACCCAGTGTAACGTGAAGTGTCCTGCTGGAACCGCT 300
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                                                                            181 CCTGGAGCTTCTACCTGTACCCCTTGTCCTCAGAAGAAGACGCTGGAGCTCAGCTAAC 240
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53830 a 58078 c 57960 g 54403 t
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                          Db 173646 reccaaggagarrecagaracarecregeaaargeacreaceceeeceeecacregeaac 173587
                                                                                                                                                                                           Qy 1116 TACCCTGATCGCTCAGTGTGCTCTGGAGTGTCCTGCTGGAACCGTGCTGACCGACGGAAC 1175
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                                                                                           1056 CIGIAAGGCTIGICCIGCTAACAAGGIGCAGGGAGCTGIGGCTACCGCTGGAGGAACCGC 1115
                                                 Indels
2.7%; Score 38.4; DB 9;
49.5%; Pred. No. 14;
tive 0; Mismatches 101;
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